

FIG.2

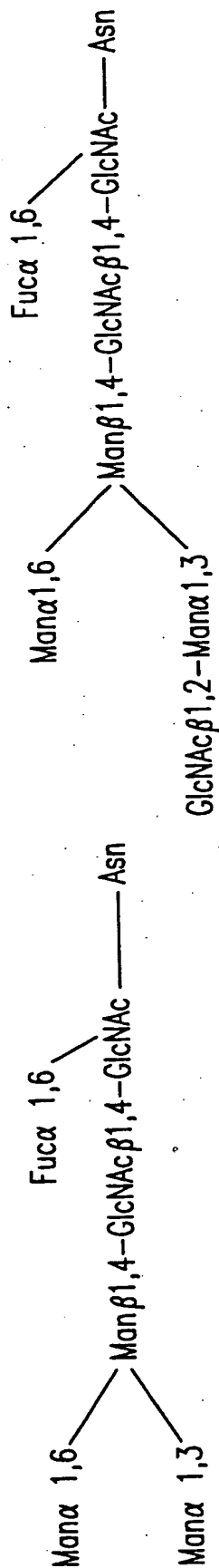


FIG. 3

FIG. 4A

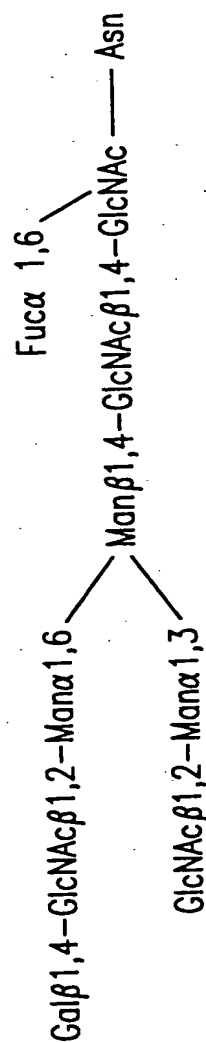


FIG. 4B

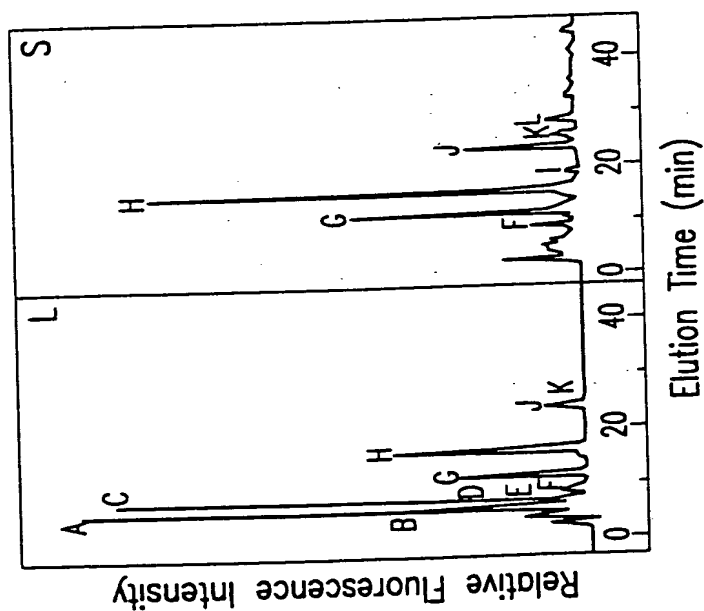


FIG.6

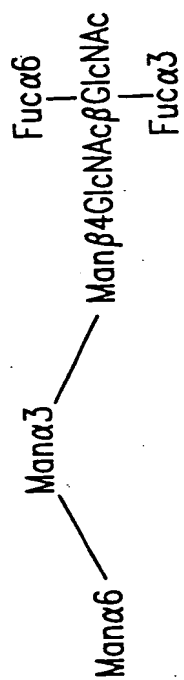


FIG.7

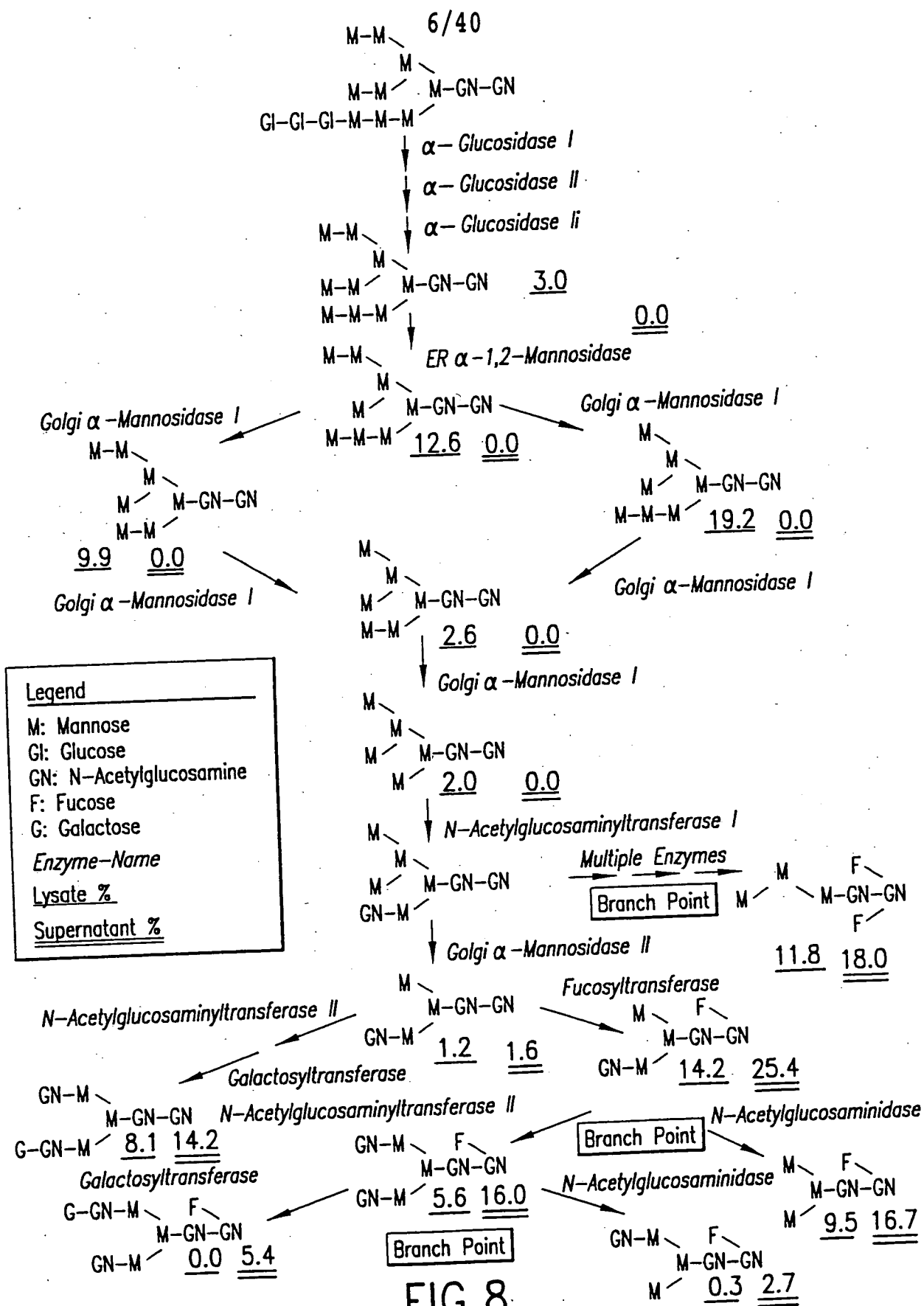


FIG.8

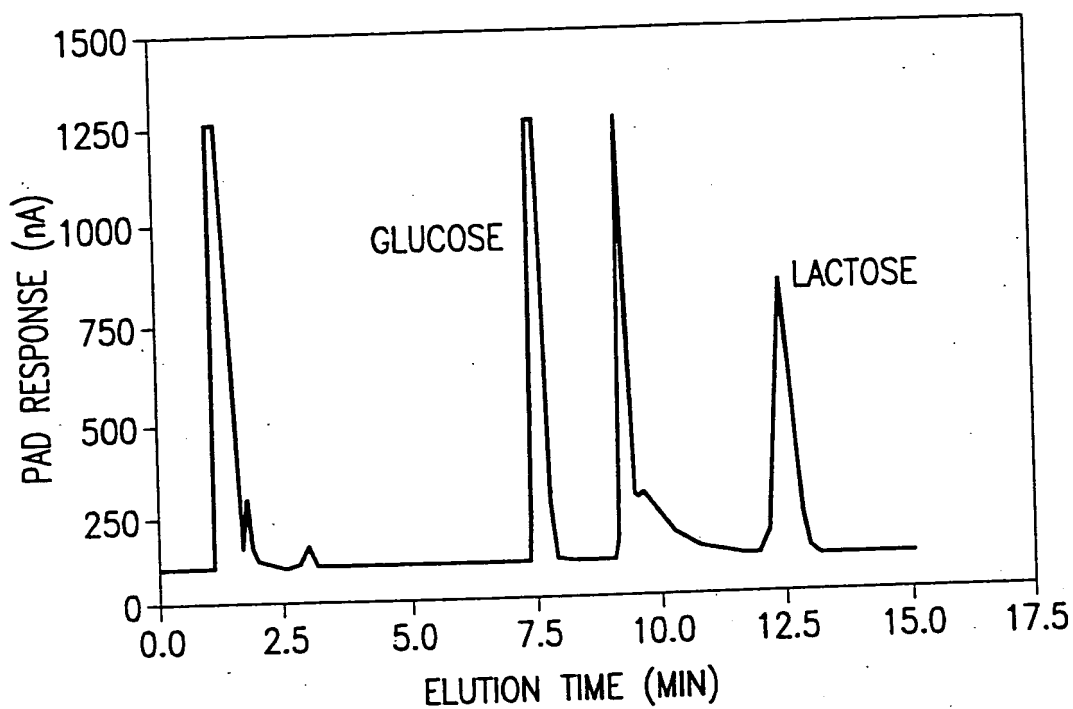


FIG. 9

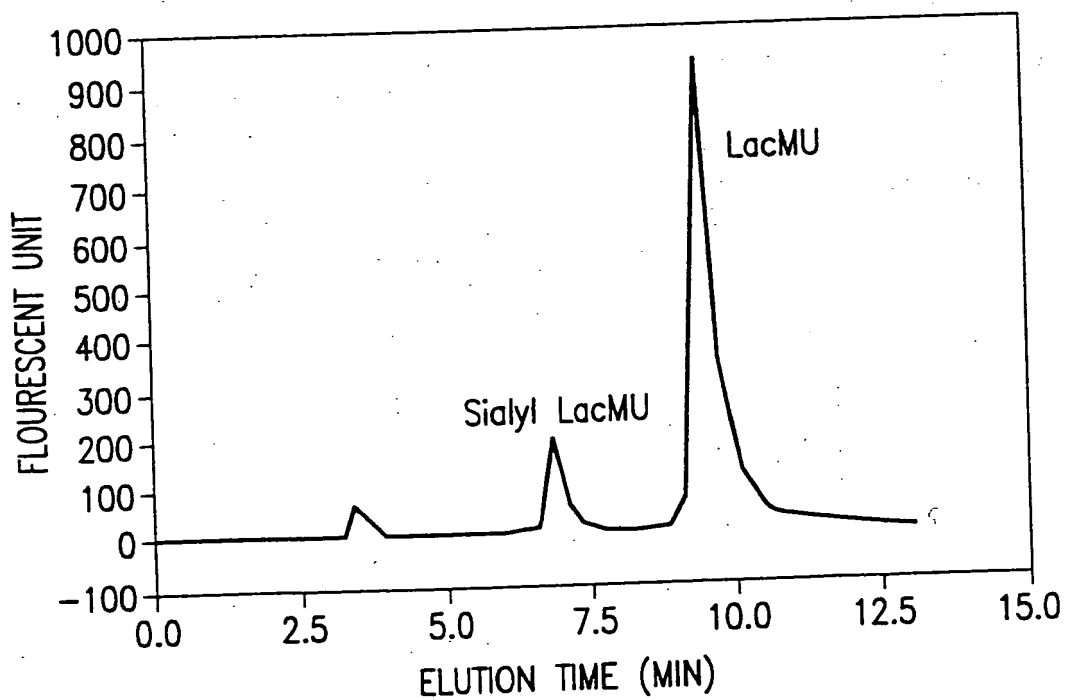


FIG. 10

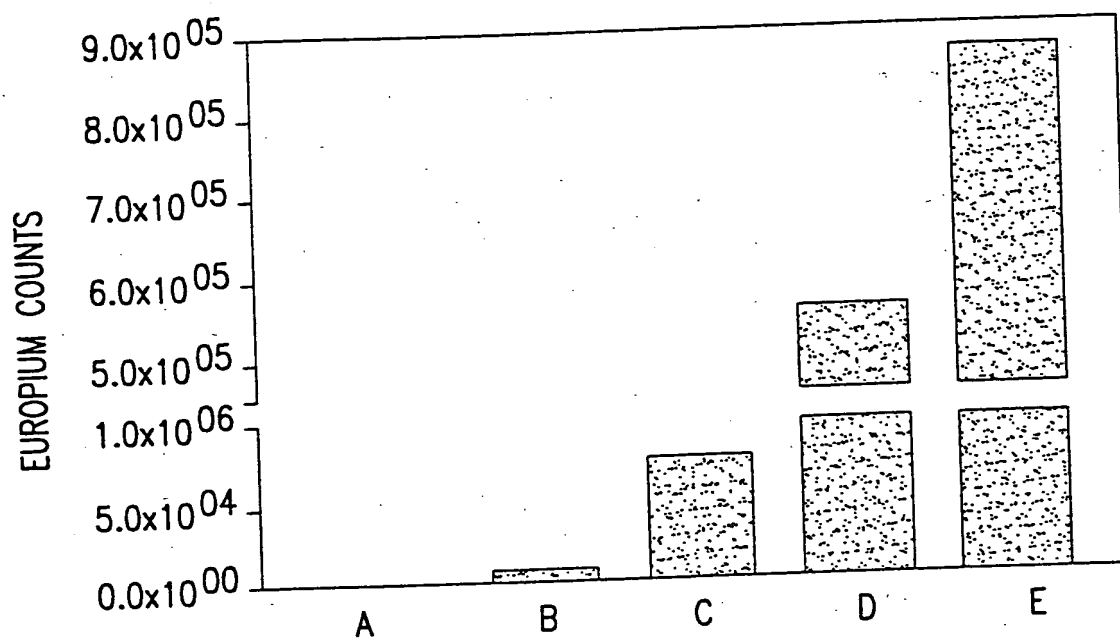


FIG. 11

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OH NH-Naph

HO OH

UDP-Gal-6Naph UDP

Dans-AE-GlcNAc

HO NHAc

HO OH

NH-Dans

GalT

FRET

Naph

Dans NH

OH NHAc

OH

FIG. 12

FIG. 12

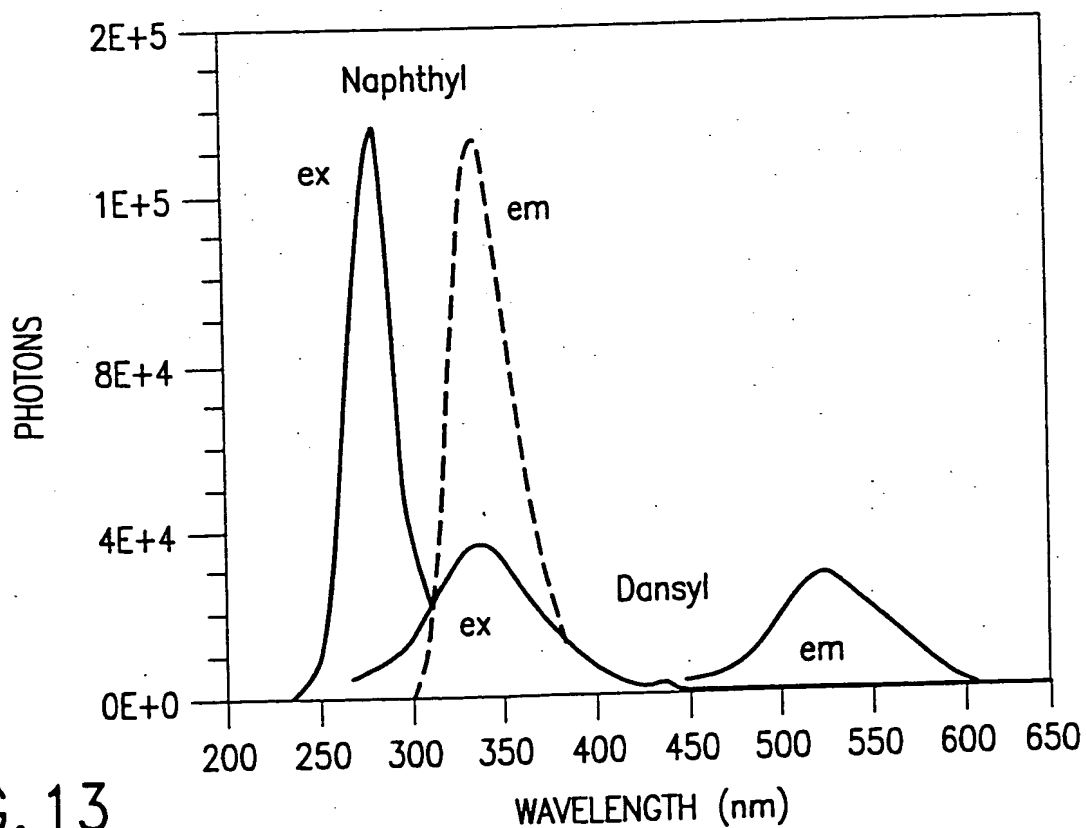


FIG. 13

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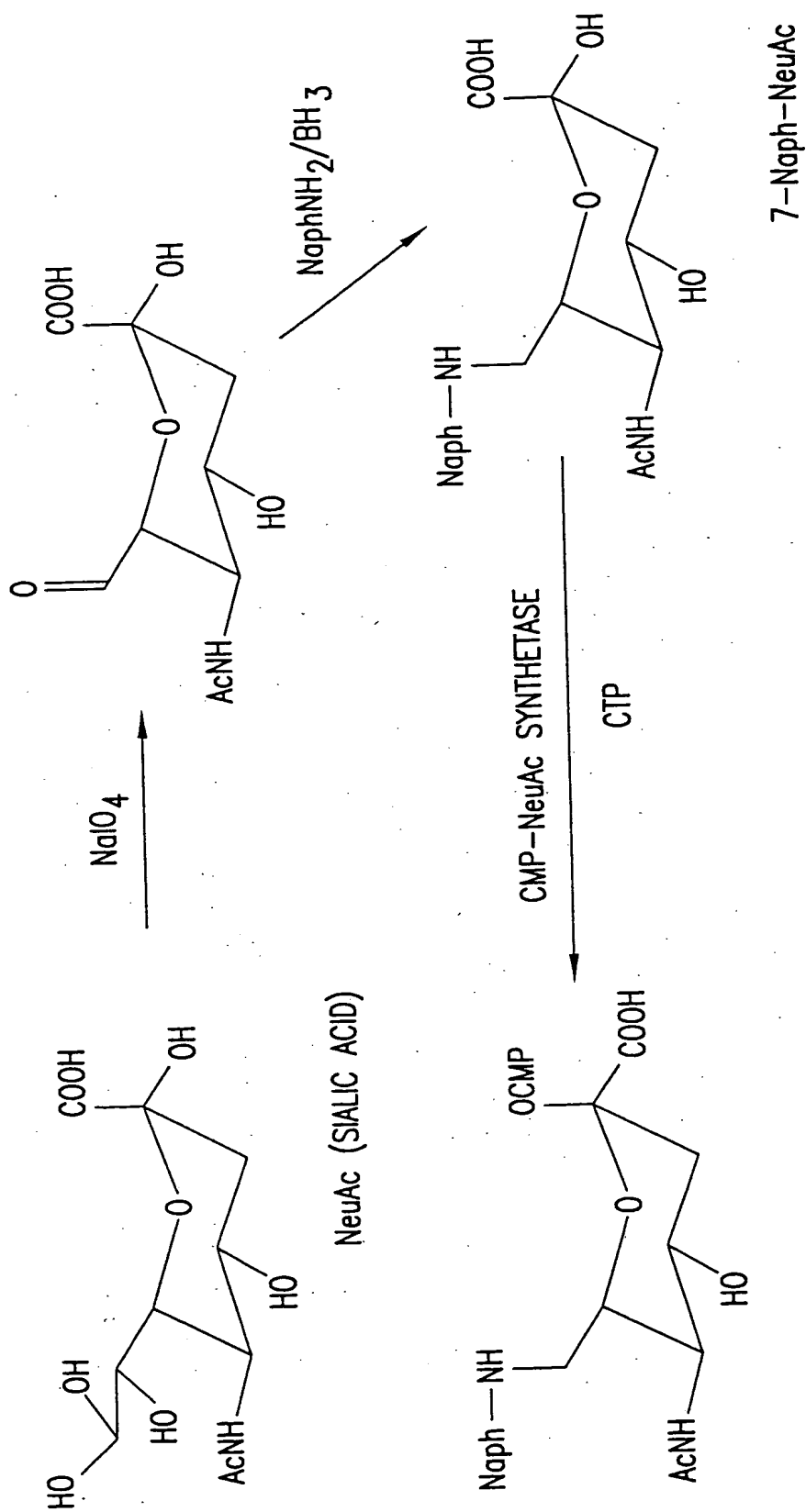


FIG. 14

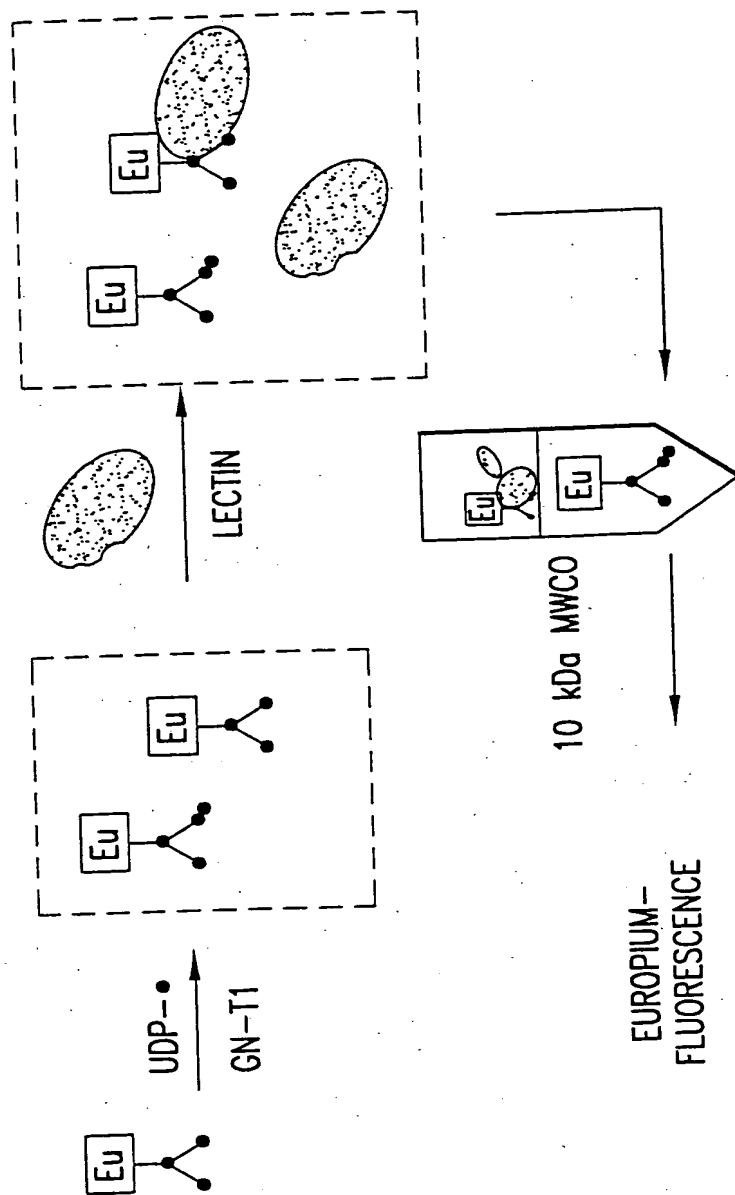


FIG. 15

433630 00000000

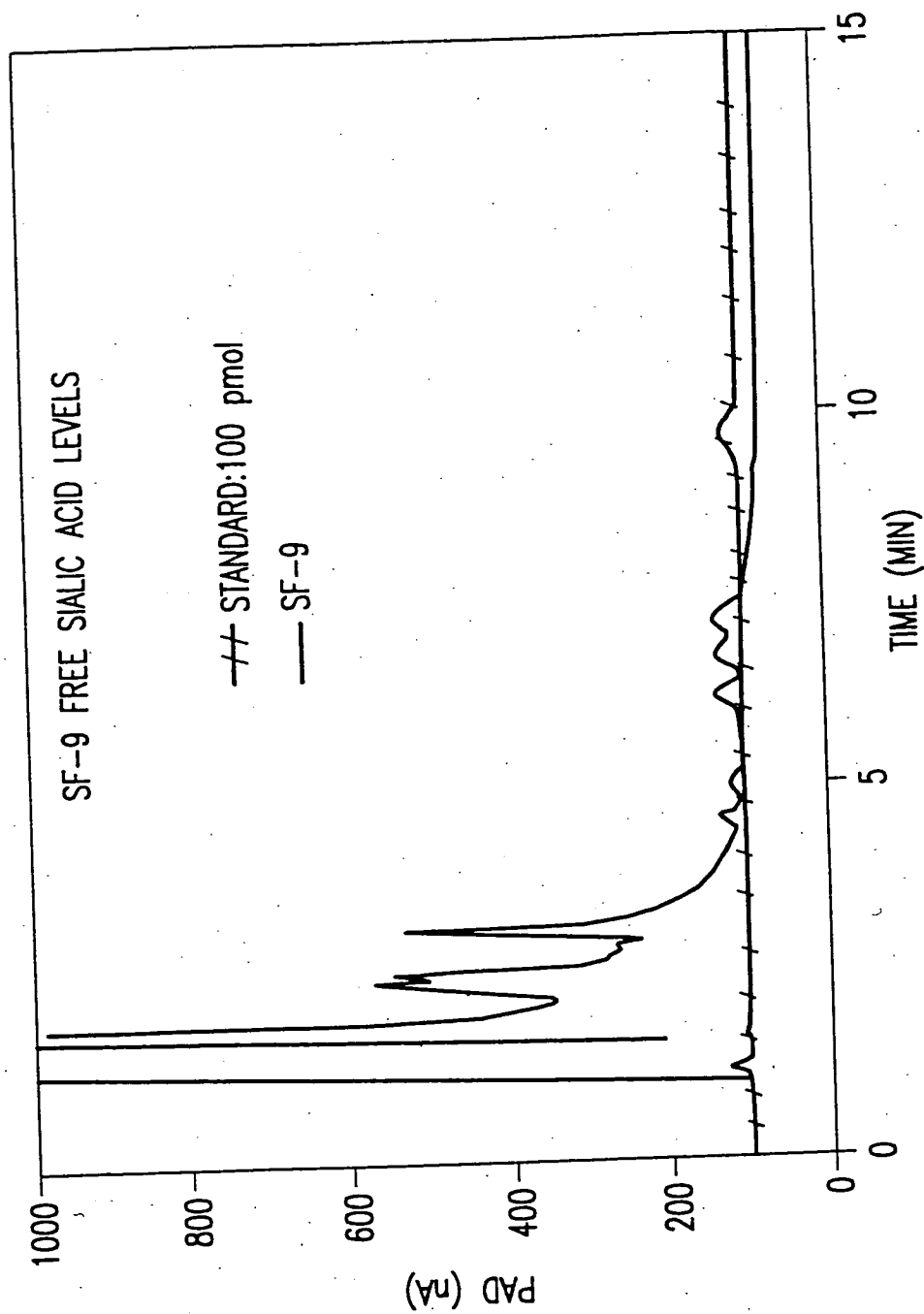


FIG. 16A

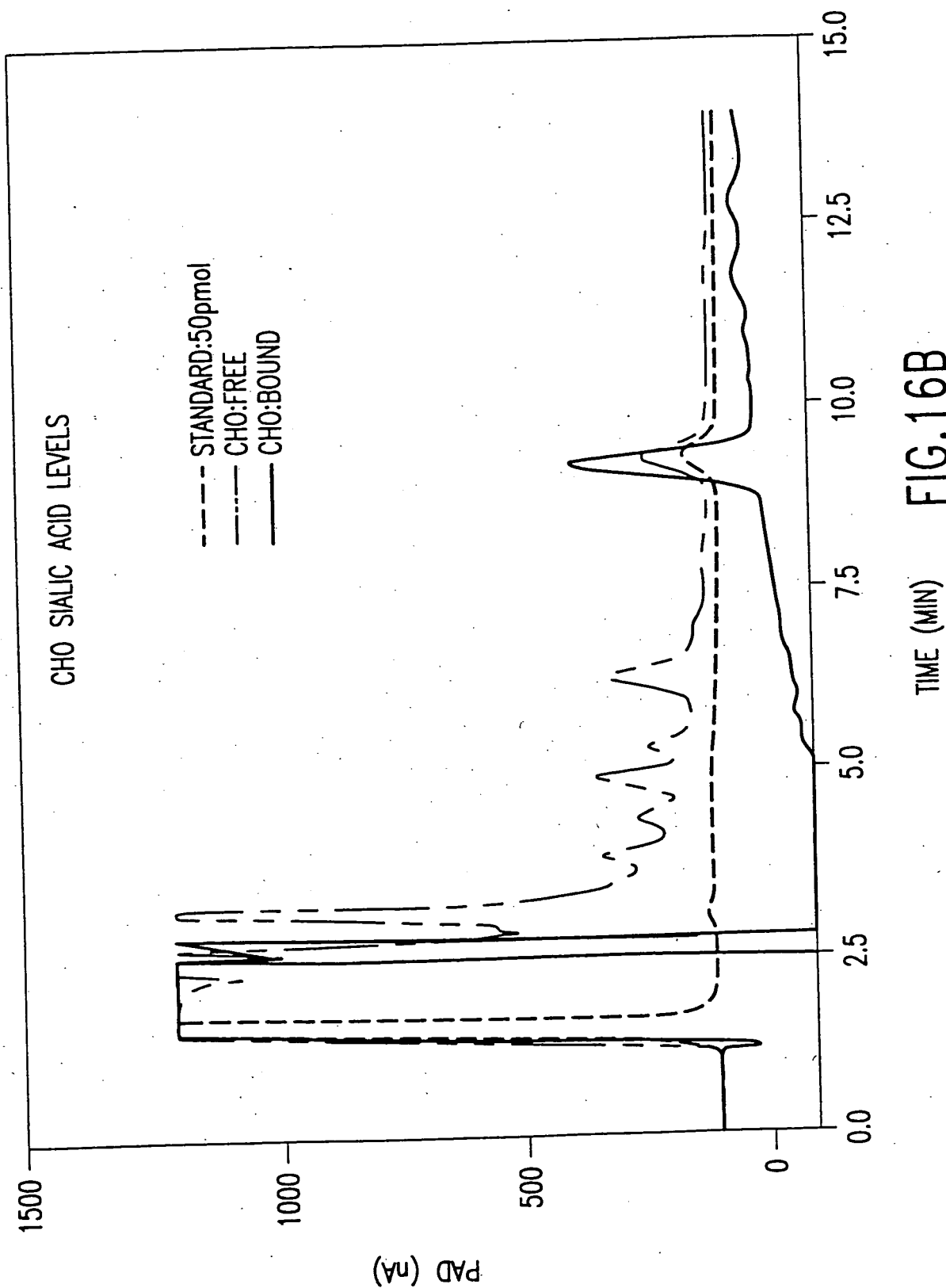


FIG.16B

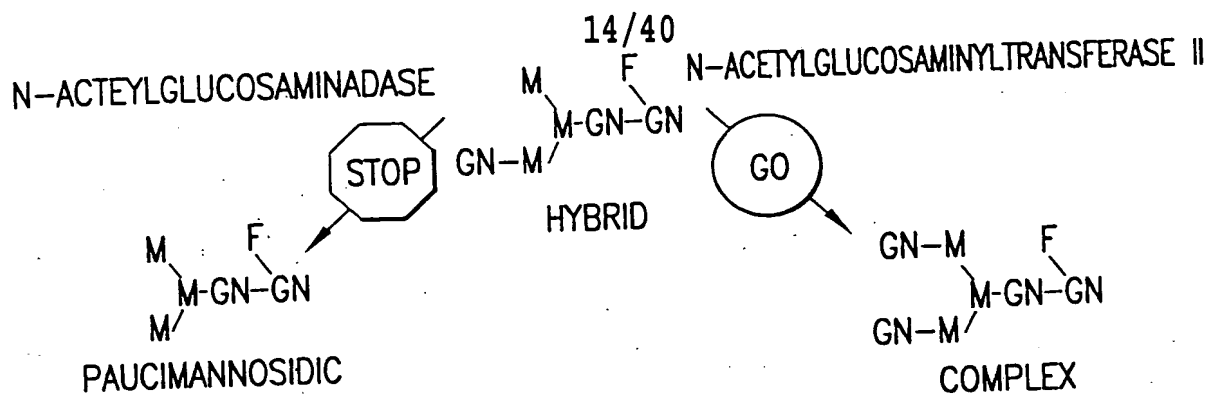
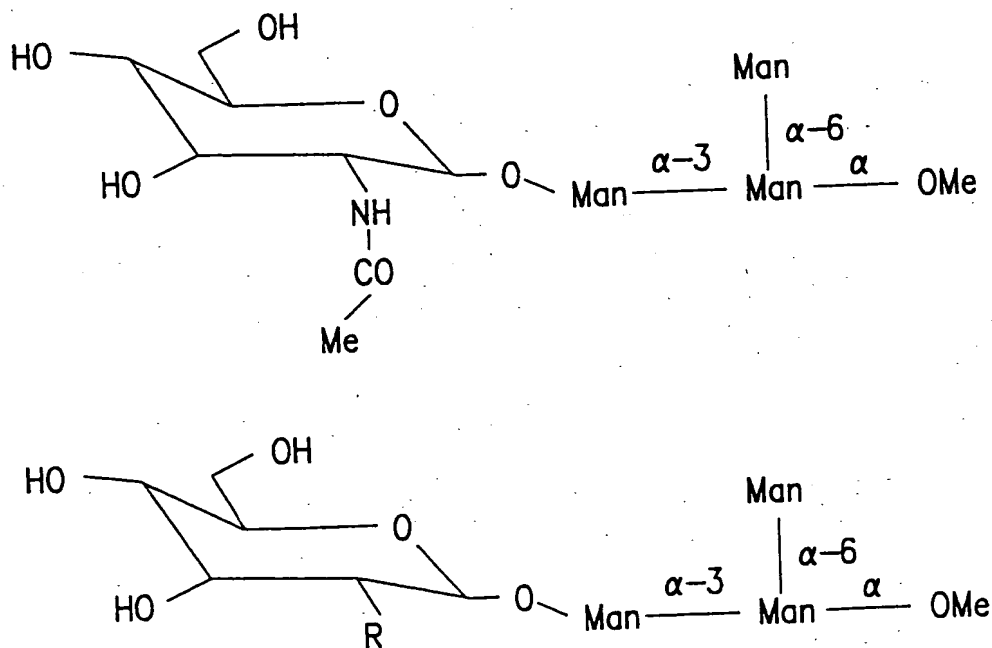


FIG. 17



R=MeCONH I I
 R=BrCH₂CONH III
 R=N₂CH₂CONH IV

FIG. 19

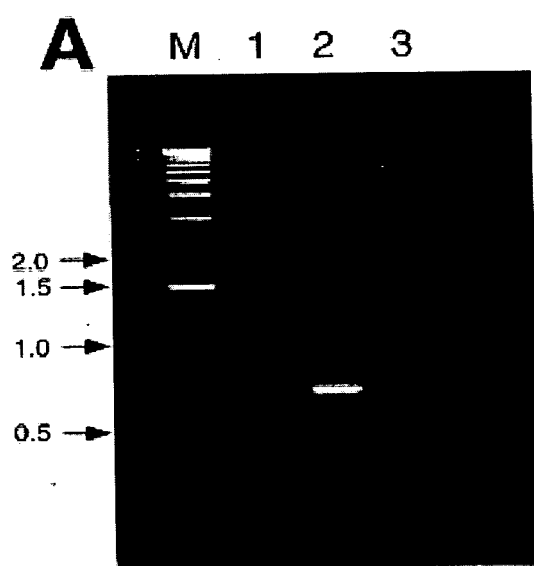


FIG. 18A

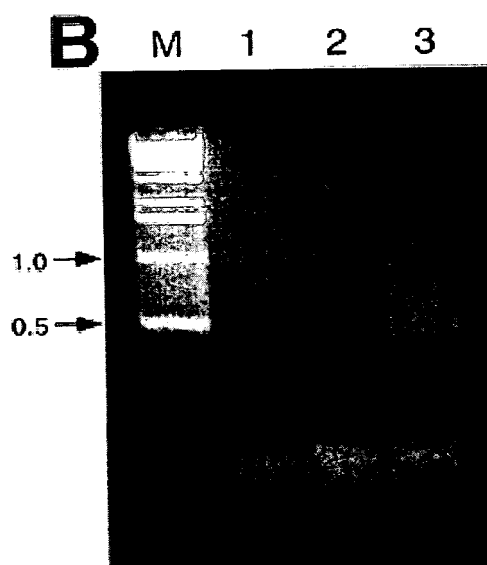


FIG. 18B

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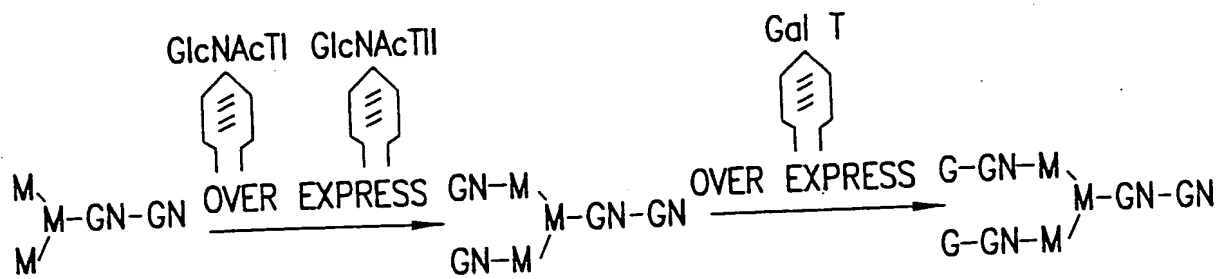


FIG. 20

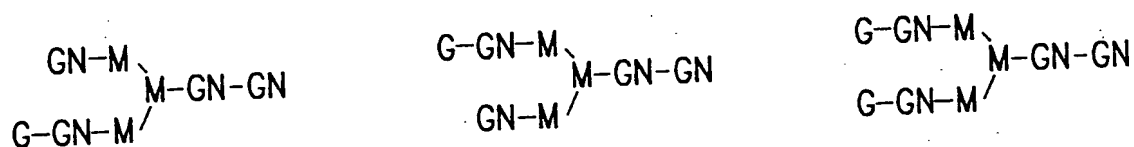
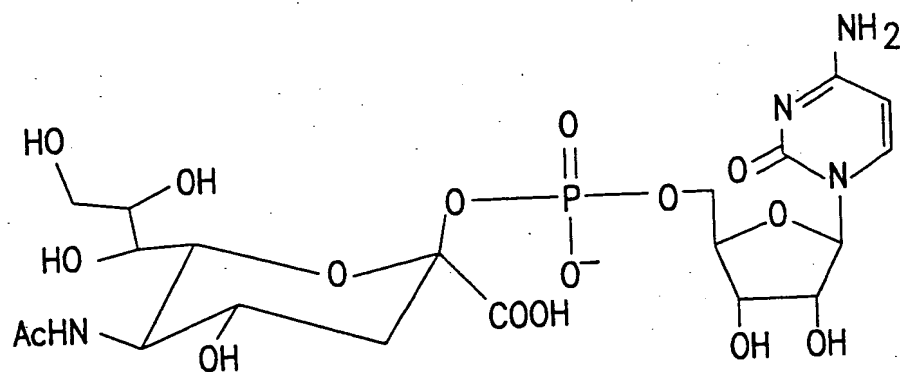
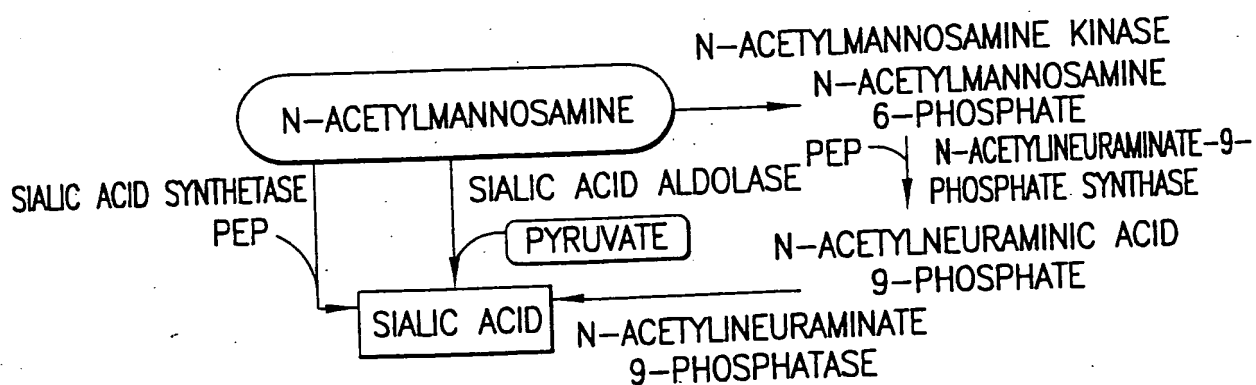
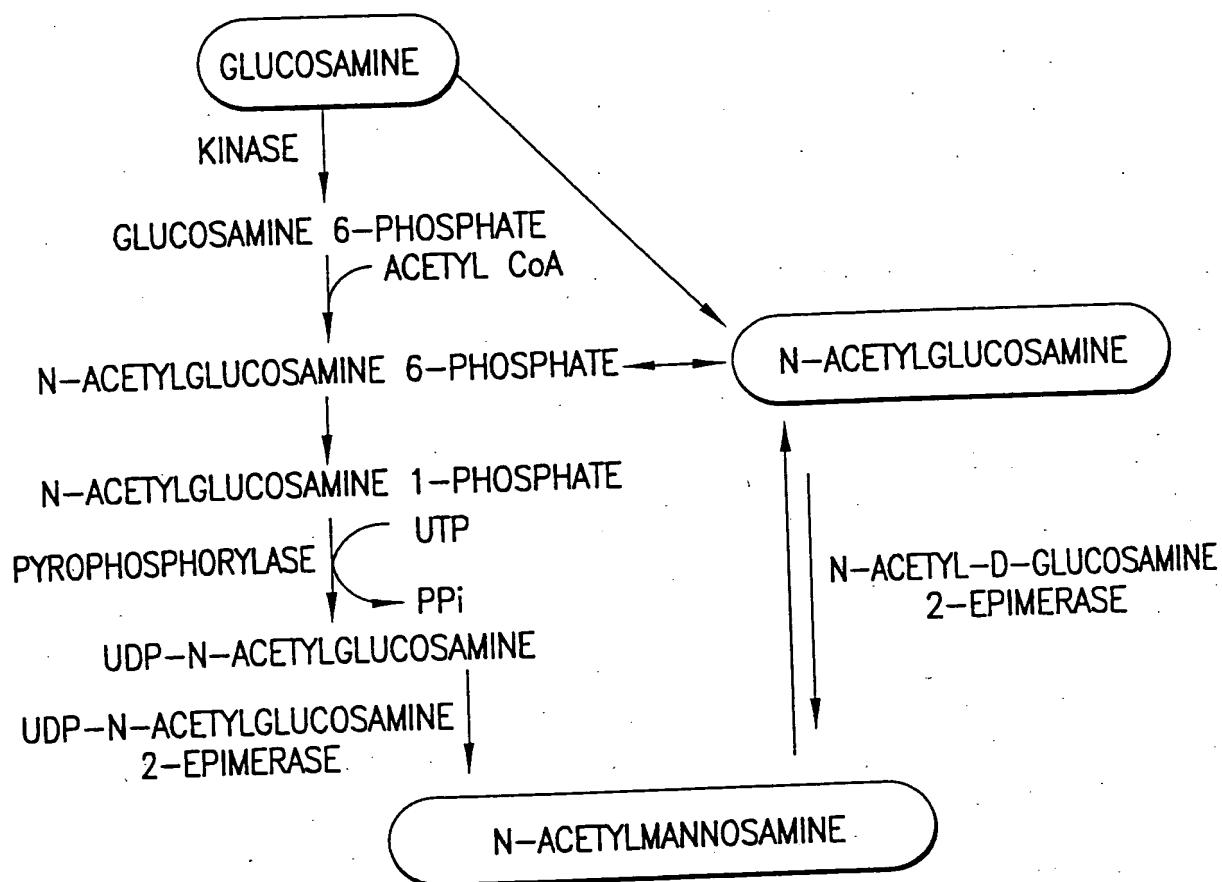


FIG. 21



CMP-SIALIC ACID

FIG. 22



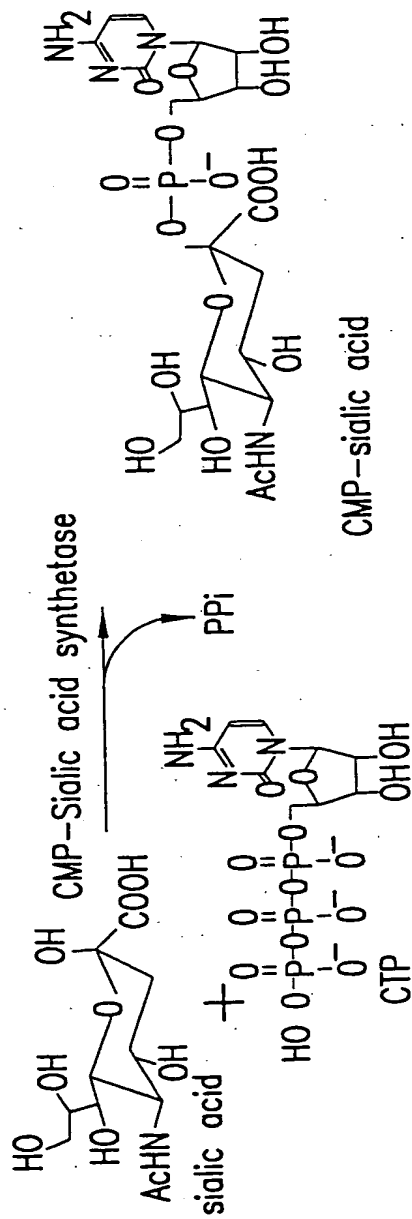


FIG.25

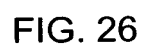


FIG. 26

ATGGCCTTCCCAAAGAAGAACTTCAGGGTCTTGTTGGCTGCAACCATCACGCCAATGACTGAGAATGGAGAAATCAA
CTTTTCAGTAATTGGTCAGTATGTGGATTATCTTGTGAAAGAACAGGGAGTGAAGAACATTTTTGTGAATGGCACAA
CAGGAGAAGGCCTGTCCCTGACCGTCTCAGAGCGTCCCGAGTTGCAGAGGAGTGGGTGACAAAAGGAAGGACAAG
CTGGATCAGGTGATAATCACGTAGGAGCACTGAGCTTGAAGGAGTCACAGGAAGTGGCCCAACATGCAGCAGAAAT
AGGAGCTGATGGCATCGCTGTCATTGCACCGTTCTTCTCAAGCCATGGACCAAAGATATCCTGATTAATTTCTAA
AGGAAGTGGCTGCTGCCGCCCTGCCCTGCCATTTTATTACTATCACATTCTGCCTTGACAGGGTAAAGATTCTGT
GCTGAGGAGTTGTTGGATGGGATTCTGGATAAGATCCCCACCTTCCAAGGGCTGAAATTCAGTGATACAGATCTCTT
AGACTTCGGGCAATGTGTTGATCAGAATCGCCAGCAACAGTTTGCTTTCTTTTTGGGGTGGATGAGCAACTGTTGA
GTGCTCTGGTGATGGGAGCAACTGGAGCAGTGGGCAGTTTGTATCCAGAGATTTATCAACTTTGTTGTCAAAGTAG
GTTTTGGAGTGTCACAGACCAAAGCCATCATGACTCTGGTCTCTGGGATTCCAATGGGGCCACCCCGGCTTCCACTG
CAGAAAGCCTCCAGCGAGTTTACTGATAGTGTGAAGCTAAAGTGAAGAGCCTGGATTTCCTTTCTTTCACTGATT
AAAGGATGGAACTTGAAGCTGGTAGCTAGTGCCTCTCTATCAAATCAGGGTTTGCACCTTGAGACATAATCTACC
TTAAATAGTGCATTTTTTCTCAGGGAATTTTAGATGAAGTGAATAAACTCTCCTAGCAAATGAAATCTCACAATA
AGCATTGAGGTACCTTTTGTGAGCCTTAAAAAGTCTTATTTTGTGAAGGGGCAAAAAGTCTAGGAGTCACAAGTCTC
AGTCATTCAATTCACAGATTTTTTGTGGAGAAATTTCTGTTTATATGGATGAAATGGAATCAAGAGGAAAAATTGTA
ATTGATTAATTCATCTGTCTTTAGGAGCTCTCATTATCTCGGTCTCTGGTTCTTAATCTATTTTAAAGTTGTCTA
ATTTTAAACCACTATAATATGTCTTCATTTTAAATAATATTCATTGGAATCTAGGAAAAGTCTGAGCTACTGCATT
TAGGCAGGCACTTTAATACCAAAGTGAACATGTCTCAACTGTATACAAGTCAAAATACACCAGCTCATTGGCTGC
TCAGTCTAACTCTAGAATGGATGCTTTTGAATTCATTTCGATG

FIG.27

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MAFPKKKLQGLVAATITPMTENGELNFSVIGQYVDYLVEKQGVKNIFVNGTTGEGLSLSVSERRQVAEEWTKGDKLDQ
VLIHVGALSLKESQELAQAHAELGADGIAVIAFFFLKPWTKDILINFLKEVAAAAPALPFYYYHIPALTGVKIRAEELLD
GILDKIPTFQGLKFSDDLDFGQCVDQNRQQQFAFLFGVDEQLLSALVMGATGAVGSFVSRDLSTLLSN.VLECHRPKP
S.LWSLGFQWAHPGFHCRKPPGSLILVLKLN.RAWISFLSLI.RMETWKLVASASLSNQGFAPLRHNL

FIG.28

ATGGACTCGGTGGAGAAGGGGGCCGCCACCTCCGTCTCCAACCCGGGGGGCGACCGTCCCGGGGCGGGCCCGGAAGCT
GCAGCGCAACTCTCGCGCGGCCAGGGCCGAGGTGGAGAAGCCCCCGACCTGGCAGCCCTAATCTGGCCCCGGGAG
GCAGCAAAGGCATCCCCCTGAAGAACATTAAGCACCTGGCGGGGTCCCGCTCATTGGCTGGGTCTCGTGGGCCCTG
GATTCAGGGCCCTTCCAGAGTGTATGGGTTTCGACAGACCATGATGAAATTGAGAATGTGGCCAAACAATTTGGTGACA
AGTTCATCGAAGAAGTTCTGAAGTTTCAAAGACAGCTCTACCTCACTAGATGCCATCATAGAATTTCTTAATTATYATA
ATGAGGKTGACATTGTAGGAAATATTCAAGCTACTTCTYCATGTTACATCCTACTGATCTTCAAAAAGTTGCAGAAATG
ATTCGAGAAGAAGGATATGATTCTGKTTTCTCTGTTGTGAGACGCCATCAGTTTCGATGGAGTGAATTCAGAAAGGAGT
TCGTGAAGTGACCGAACCTCTGAATTTAAATCCAGCTAAACGGCCTCGTCGACAAGACTGGGATGGAGAATTATATGAAA
ATGGCTCATTTTATTTTGCTAAAAGACATTTGATAGAGATGGGTTACTTGCAGGTGGAATGGCATACTACGAAATGC
GAGCTGGAACATAGTGTGGATATAGATGTGGATATTGATTGGCCTATTGCAGAGCAAAGAGTATTAAGATATGGCTATTT
TGGCAAAGAGAAGCTTAAGGAAATAAACTTTTGGTTTGAATATTGATGGATGTCTCACCAATGGCCACATTTATGTAT
CAGGAGACCAAAAAGAAATAATATCTTATGATGTAAAAGATGCTATTGGGATAAGTTTATTAAGAAAAGTGGTATTGAG
GTGAGGCTAATCTCAGAAAGGCCGTGTTCAAAGCAGACGCTGTCTCTTTAAAAGTGGATTGCAAAATGGAAGTCAGTGT
ATCAGACAAGCTAGCAGTTGTAGATGAATGGAGAAAAGAAATGGGCTGTGCTGGAAGAAGTGGCATACTTGGAAATG
AAGTGTCTGATGAAGAGTGTGTAAGAGAGTGGGCTAAGTGGCGCTCTGCTGATGCCTGTTCTACGCCCAGAAGGCT
GTTGGATACATTTGCAAAATGTAATGGTGGCGGTGGTCCCATCCGAGAATTTCAGAGCACATTTGCCTACTAATGAAAA
AGTTAATAATTCATGCCAAAAATAG

FIG.29

MDSVEKGAATSVSNPRGRPSRGRPPKLQRNSRGGQGRGVEKPPHLAALILARGGSKGIPLNKIKHLACVPLIGWVLRAL
DSGAFQSVWVSTDHDEIENVAKQFQAQVHRSSEVSKDSSTSLDAIEFLNYXNEXDIVGNIQATSXCLHPTDLQKVAEM
IREEGYDSXFSVVRHQRWSEIQKGVREVTPLNLPKRPRRQDWDGELYENGsfYfAKRHLIEMGYLQGGKWHHTKC
ELEHSVDIDVDIDWPIAEQRLRYCYFGKEKLKEIKLLVCNIDGCLTNGHIYVSGDQKEIISYDVKDAIGISLLKKSGLIE
VRLISERACSKQTLSSLKLDCKMEVSVDKLAVIDEWRKEMGLCWKEVAYLGNEVSDEECLKRVGLSGAPADACSYAQKA
VGYICKCNGGRGAIREFAEHICLLMEKVNNSCQK.

FIG.30

ATGCCGCTGGAGCTGGAGCTGTGTCCCGGGCGCTGGGTGGGCGGGCAACACCCGTGCTTCATCATTGCCGAGATCGGCCA
 GAACCACCAGGGCGACCTGGACGTAGCCAAGCCCATGATCCGCATGGCCAAGGAGTG TGGGCTGATTGTGCCAAGTTCC
 AGAAGAGTGAGCTAGAATTCAGTTTAAATCGAAAGCCTTGGAGAGGCCATACACCTCGAAGCATTCTGGGGGAAGACC
 TACGGGGAGCACAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGGTACGCCGAGGAGGTGGGAT
 CTTCCTCACTGCCTCTGGCATGGATGAGATGGCAGTTGAATTCCTGCATGAAGTGAATGTTCCATTTTCAAAGTTGGAT
 CTGGAGACACTAATAATTTTCCTTATCTGGAAAAGACAGCCAAAAAAGGTGCGCCCAATGGTGATCTCCAGTGGGATGCAG
 TCAATGGACACCATGAAGCAAGTTTATCAGATCGTGAAGCCCTCAACCCCAACTTCTGCTTCTTGCAAGTGTACCAGCGC
 ATACCCGCTCCAGCCTGAGGACGTCAACCTGCGGGTCATCTCGGAATATCAGAAGCTCTTCTGACATTCACATAGGGT
 ATTCTGGGCATGAAACAGGCATAGCGATATCTGTGGCCGAGTGGCTCTGGGGGCAAGGTGTTGGAACGTCACATAACT
 TTGGACAAGACCTGGAAGGGGAGTGACCACTCGGCCTCGCTGGAGCCTGGAGAAGTGGCCGAGCTGGTGGCGTCAGTGGC
 TCTTGTTGGAGCGTGCCCTGGGCTCCCCAACCAAGCAGCTGCTGCCCCTGTGAGATGGCCTGCAATGAGAAGCTGGGCAAGT
 CTGTGGTGGCCAAAGTGAATAATTCGGAAGGCACCATCTAACAATGGACATGCTCACCGTGAAGGTGGGTGAGCCCAA
 GCCTATCTCTGAAGACATCTTAAATCTAGTGGGCAAGAAGTCTGCTCACTGTTGAAGAGGATGACACCATCATGGA
 AGAATTGGTAGATAATCATGGCAAAAAAATCAAGTCTTAA

FIG.31

MPLLELCPRWVGQHPCF I IAE I GQNHQGDLDVAKRM I RMAKECGADCAKFQKSELEFKFNRKALERPYSKHSWCKT
 YGEHKKRHLF SHDQYRELQRYAEEVG IFF TASGMDMAVEFLHELNPFFKVGSGDTNNFPYLEKTAKKGRPMV I SSGMQ
 SMDTMKQVYQ I VKPLNPNFCFLQCT SAYPLQPEDVNL RV I SEYQKLPD I P I GYSGHETG I A I SVAVALGAKVLERH I T
 LDKTWKGS DHSASLEPGELAE L VRSVRLVERALGSPTKQLLPCEMACNEKL GKS VVAKV I PEGT I L TMDMLTVKVGE PK
 AYPPED I FNLVGKKVLVTVEEDT I MEELVDNHGKK I KS

FIG.32

Peak/code (G.U. ODS, amide)	PA-oligosaccharide structure	Secreted hTf (mol%)	
		-GalT	+GalT
A/M8.1 (4.9,9.0)	$ \begin{array}{c} \text{Man}\alpha 2-\text{Man}\alpha 6 \\ \quad \quad \quad \diagdown \quad \diagup \\ \quad \quad \text{Man}\alpha 3 \quad \text{Manb} 4-\text{GlcNAcb} 4-\text{GlcNAc} \\ \quad \quad \diagup \quad \diagdown \\ \text{Man}\alpha 2-\text{Man}\alpha 2-\text{Man}\alpha 3 \end{array} $	3.9	10.1
B1/M7.2 (5.1,8.1)	$ \begin{array}{c} \text{Man}\alpha 2-\text{Man}\alpha 6 \\ \quad \quad \quad \diagdown \quad \diagup \\ \quad \quad \text{Man}\alpha 3 \quad \text{Manb} 4-\text{GlcNAcb} 4-\text{GlcNAc} \\ \quad \quad \diagup \quad \diagdown \\ \text{Man}\alpha 2-\text{Man}\alpha 3 \end{array} $	2.3	5.5
B2/M9.1 (5.2,9.7)	$ \begin{array}{c} \text{Man}\alpha 2-\text{Man}\alpha 6 \\ \quad \quad \quad \diagdown \quad \diagup \\ \quad \quad \text{Man}\alpha 2-\text{Man}\alpha 3 \quad \text{Manb} 4-\text{GlcNAcb} 4-\text{GlcNAc} \\ \quad \quad \diagup \quad \diagdown \\ \text{Man}\alpha 2-\text{Man}\alpha 2-\text{Man}\alpha 3 \end{array} $	11.6	23.5
C/M7.1 (5.8,8.0)	$ \begin{array}{c} \text{Man}\alpha 6 \\ \quad \quad \quad \diagdown \quad \diagup \\ \quad \quad \text{Man}\alpha 3 \quad \text{Manab} 4-\text{GlcNAcb} 4-\text{GlcNAc} \\ \quad \quad \diagup \quad \diagdown \\ \text{Man}\alpha 2-\text{Man}\alpha 2-\text{Man}\alpha 3 \end{array} $	2.3	5.5
D/M6.1 (6.1,7.1)	$ \begin{array}{c} \text{Man}\alpha 6 \\ \quad \quad \quad \diagdown \quad \diagup \\ \quad \quad \text{Man}\alpha 3 \quad \text{Manb} 4-\text{GlcNAcb} 4-\text{GlcNAc} \\ \quad \quad \diagup \quad \diagdown \\ \text{Man}\alpha 2-\text{Man}\alpha 2-\text{Man}\alpha 3 \end{array} $	4.7	13.4

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FIG. 33A

Peak/code (G.U. ODS, amide)	PA-oligosaccharide structure	Secreted hTf (mol%)	
		-GalT	+GalT
E1/M9.2 (6.3,10.3)	$ \begin{array}{c} \text{Man}_2\text{-Man}_6 \\ \text{Man}_2\text{-Man}_3 \quad \text{Man}_6 \\ \text{Glc}_3\text{-Man}_2\text{-Man}_2\text{-Man}_3 \quad \text{Man}_4\text{-GlcNAcb}_4\text{-GlcNAc} \end{array} $	1.3	3.7
E2/M8.2 (6.4,8.5)	$ \begin{array}{c} \text{Man}_6 \\ \text{Man}_2\text{-Man}_3 \quad \text{Man}_6 \\ \text{Man}_2\text{-Man}_2\text{-Man}_3 \quad \text{Man}_4\text{-GlcNAcb}_4\text{-GlcNAc} \end{array} $	0.3	0.8
F1/M5.1 (7.2,6.2)	$ \begin{array}{c} \text{Man}_6 \\ \text{Man}_3 \quad \text{Man}_6 \\ \text{Man}_3 \quad \text{Man}_4\text{-GlcNAcb}_4\text{-GlcNAc} \end{array} $	4.6	2.4
F2/000.1 (7.4,4.3)	$ \begin{array}{c} \text{Man}_6 \\ \text{Man}_3 \quad \text{Man}_6 \\ \text{Man}_3 \quad \text{Man}_4\text{-GlcNAcb}_4\text{-GlcNAc} \end{array} $	9.0	5.8
F3/100.2 (7.4,4.7)	$ \begin{array}{c} \text{Man}_6 \\ \text{GlcNAcb}_2\text{-Man}_3 \quad \text{Man}_6 \\ \text{Man}_4\text{-GlcNAcb}_4\text{-GlcNAc} \end{array} $	6.5	3.1
G1/M6.10 (7.9,6.8)	$ \begin{array}{c} \text{Man}_6 \\ \text{Man}_2\text{-Man}_3 \quad \text{Man}_6 \\ \text{Man}_4\text{-GlcNAcb}_4\text{-GlcNAc} \end{array} $	1.1	1.1

Secreted hTf

(mol%)

-GalT +GalT

PA-oligosaccharide
structure

Peak/code
(G.U. ODS, amide)

G2/100.4 (8.0,5.7)	$ \begin{array}{c} \text{Man}_6 \\ \diagup \quad \diagdown \\ \text{Galb4-GlcNAcb2-Mana3} \quad \text{Manb4-GlcNAcb4-GlcNAc} \end{array} $	nd	5.0
H/000.1FF (8.5,5.5)	$ \begin{array}{c} \text{Fuca 6} \\ \\ \text{Man}_6 \quad \text{Fuca 3} \\ \diagup \quad \diagdown \\ \text{Manb4-GlcNAcb4-GlcNAc} \\ \text{Mana3} \end{array} $	5.9	1.7
I/100.4FF (8.9,7.0)	$ \begin{array}{c} \text{Fuca 6} \\ \\ \text{Man}_6 \quad \text{Fuca 3} \\ \diagup \quad \diagdown \\ \text{Manb4-GlcNAcb4-GlcNAc} \\ \text{Galb4-GlcNAcb2-Mana3} \end{array} $	nd	1.3
J1/010.0 (7.2,6.2)	$ \begin{array}{c} \text{Fuca 6} \\ \\ \text{Man}_6 \quad \text{Fuca 3} \\ \diagup \quad \diagdown \\ \text{Manb4-GlcNAcb4-GlcNAc} \end{array} $	23.4	4.0
J2/010.1 (10.2,4.7)	$ \begin{array}{c} \text{Fuca 6} \\ \\ \text{Man}_6 \quad \text{Fuca 3} \\ \diagup \quad \diagdown \\ \text{Manb4-GlcNAcb4-GlcNAc} \end{array} $	15.7	6.1

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FIG.33C

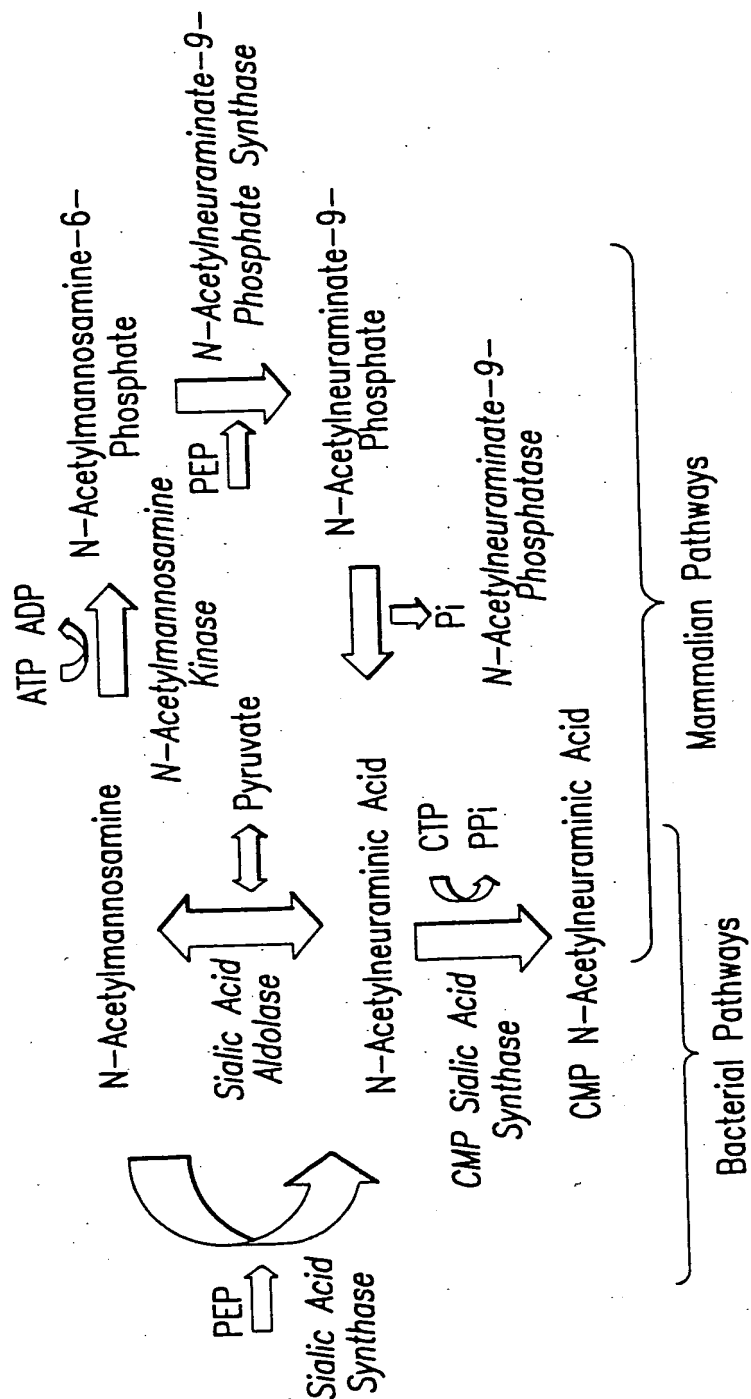


FIG.34

	10	20	30	40	50	60
1	CGG ACC CAG ACT GGT AGT GCA GGC TTT GGA CCC CGA GCC GCT GCA ATG CCG CTG GAG CTG	60				
1					M P L E L	5
	70	80	90	100	110	120
61	GAG CTG TGT CCC GGG CGC TGG GTG GGC GGG CAA CAC CCG TGC TTC ATC AIT GCC GAG ATC	120				
6	E L C P G R W V G G Q H P C F I I A E I	25				
	130	140	150	160	170	180
121	GGC CAG AAC CAC CAG GGC GAC CTG GAC GTA GCC AAG CGC ATG ATC CGC ATG GCC AAG GAG	180				
26	G Q N H Q G D L D V A K R M I R M A K E	45				
	190	200	210	220	230	240
181	TGT GGG GCT GAT TGT GCC AAG TTC CAG AAG AGT GAG CTA GAA TTC AAG TTT AAT CCG AAA	240				
46	C G A D C A K F Q K S E L E F K F N R K	65				
	250	260	270	280	290	300
241	GCC TTG GAG AGG CCA TAC ACC TCG AAG CAT TCC TGG GGG AAG ACG TAC GGG GAG CAC AAA	300				
66	A L E R P Y T S K H S W G K T Y G E H K	85				
	310	320	330	340	350	360
301	CGA CAT CTG GAG TTC AGC CAT GAC CAG TAC AGG GAG CTG CAG AGG TAC GCC GAG GAG GTT	360				
86	R H L E F S H D Q Y R E L Q R Y A E E V	105				
	370	380	390	400	410	420
361	GGG ATC TTC TTC ACT GCC TCT GGC ATG GAT GAG ATG GCA GTT GAA TTC CTG CAT GAA CTG	420				
106	G I F F T A S G M D E M A V E F L H E L	125				
	430	440	450	460	470	480
421	AAT GTT CCA TTT TTC AAA GTT GGA TCT GGA GAC ACT AAT AAT TTT CCT TAT CTG GAA AAG	480				
126	N V P F F K V G S G D T N N F P Y L E K	145				

FIG. 35A

490 500 510 520 530 540
 481 ACA GCC AAA AAA GGT CGC CCA ATG GTG ATC TCC AGT GGG ATG CAG TCA ATG GAC ACC ATG 540
 146 T A K K G R P M V I S S G M Q S M D T M 165
 550 560 570 580 590 600
 541 AAG CAA GTT TAT CAG ATC GTG AAG CCC CTC AAC CCC AAC TTC TGC TTC TTG CAG TGT ACC 600
 166 K Q V Y Q I V K P L N P N F C F L Q C T 185
 610 620 630 640 650 660
 601 AGC GCA TAC CCG CTC CAG CCT GAG GAC GTC AAC CTG CCG GTC ATC TCG GAA TAT CAG AAG 660
 186 S A Y P L Q P E D V N L R V I S E Y Q K 205
 670 680 690 700 710 720
 661 CTC TTT CCT GAC ATT CCC ATA GGG TAT TCT GGG CAT GAA ACA GGC ATA GCG ATA TCT GTG 720
 206 L F P D I P I G Y S G H E T G I A I S V 225
 730 740 750 760 770 780
 721 GCC GCA GTG GCT CTG GGG GCC AAG GTG TTG GAA CGT CAC ATA ACT TTG GAC AAG ACC TGG 780
 226 A A V A L G A K V L E R H I T L D K T W 245
 790 800 810 820 830 840
 781 AAG GGG AGT GAC CAC TCG GCC TCG CTG GAG CCT GGA GAA CTG GCC GAG CTG GTG CCG TCA 840
 246 K G S D H S A S L E P G E L A E L V R S 265
 850 860 870 880 890 900
 841 GTG CGT CTT GTG GAG CGT GCC CTG GGC TCC CCA ACC AAG CAG CTG CTG CCC TGT GAG ATG 900
 266 V R L V E R A L G S P T K Q L L P C E M 285
 910 920 930 940 950 960
 901 GCC TGC AAT GAG AAG CTG GGC AAG TCT GTG GTG GCC AAA GTG AAA ATT CCG GAA GGC ACC 960
 286 A C N E K L G K S V V A K V K I P E G T 305

FIG. 35B

30/40

	970	980	990	1000	1010	1020	
961	ATT	CTA	ACA	ATG	GAC	ATG	CTC
306	I	L	T	M	D	M	L
	1030	1040	1050	1060	1070	1080	
1021	GAC	ATC	TTT	AAT	CTA	GTG	GGC
326	D	I	F	N	L	V	G
	1090	1100	1110	1120	1130	1140	
1081	ATG	GAA	GAA	TTG	GTA	GAT	AAT
346	M	E	E	L	V	D	N
1141	CTC	TGA	1146				

FIG. 35C

1 MPLELELCPRWVGQHPFCFIIAEIGQNHQGDLDVAKRMIRMAKECGADCAKFQKSELEF
 | | | | | | | | | | | | | | | | | |
 1 MS-----NIYIVAEIGCNHNGSVDIAREMILKAKEAGVNAVKFQTFKADK

 61 KFN RKALERP YTSKHSWG-KTYGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAV
 | | | | | | | | | | | | | | | | | |
 46 LISAIAPKAEYQIKNTGELESQLEMTKKLEMKYDDYLHLM EYAVSLNLDVFSTPFDEDSI

 120 EFLHELNV PFFKVGSGDTNNFPYLEKTAK---KGRPMVISSGMQSDMTMKQ---VYQIVK
 | | | | | | | | | | | | | | | | | |
 106 DFLASLKQKIWKIPSGELLNLPYLEKIAKLPIPDKKIIISTGMATIDEIKQSVSIFINN K

 174 PLNP NFCFLQCT SAYPLQPEDVNL RVI SEYQKLFPDIPIGYSGHETGIAISVAAVALGAK
 | | | | | | | | | | | | | | | | | |
 166 VPVGNITILHCNTEYPTPFEDVNLNAINDLK KHFPKNNIGFSDHSSGFYAAIAAVPYGIT

 234 VLERHITLDK TWKGS DHSASLEPGELAE LVR SVRLVERALGSPTKQLLPCEMACNEKL GK
 | | | | | | | | | | | | | | | | | |
 226 FIEKHFTLDKSMSPDHLASIEPDELKHL CIGVRCVEKSLGSNSKVVTASERKNKIVARK

 294 SVVAKVKIPEGTIL TMDMLTVKVGE PKAYPPEDIFNLVGKKVLVTVEEDDTIMEELVDNH
 | | | | | | | | | | | | | | | | | |
 286 SIIAKTEIKKGEVFSEKNITTKRP-GNGISPMEWYNLLGK-----IAEQDFIPDELI IHS

 354 G-KKIKS
 |
 340 EFKNQGE

FIG. 35D

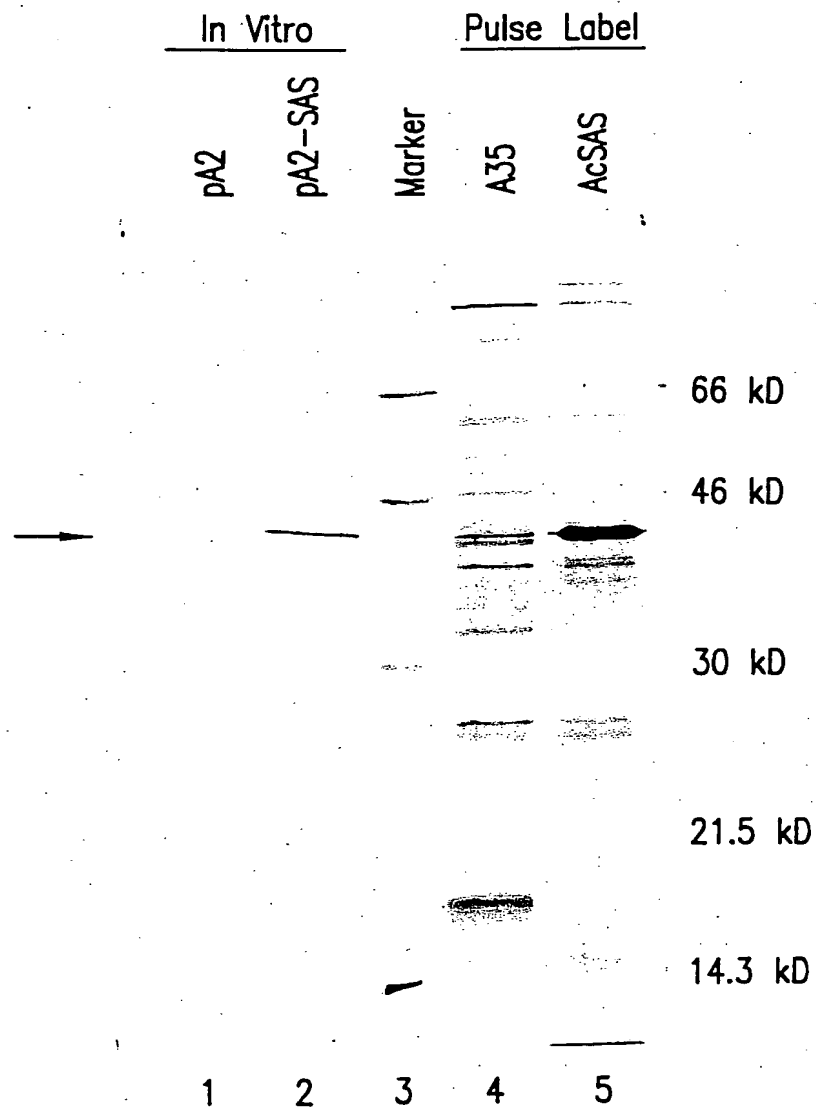


FIG.36A

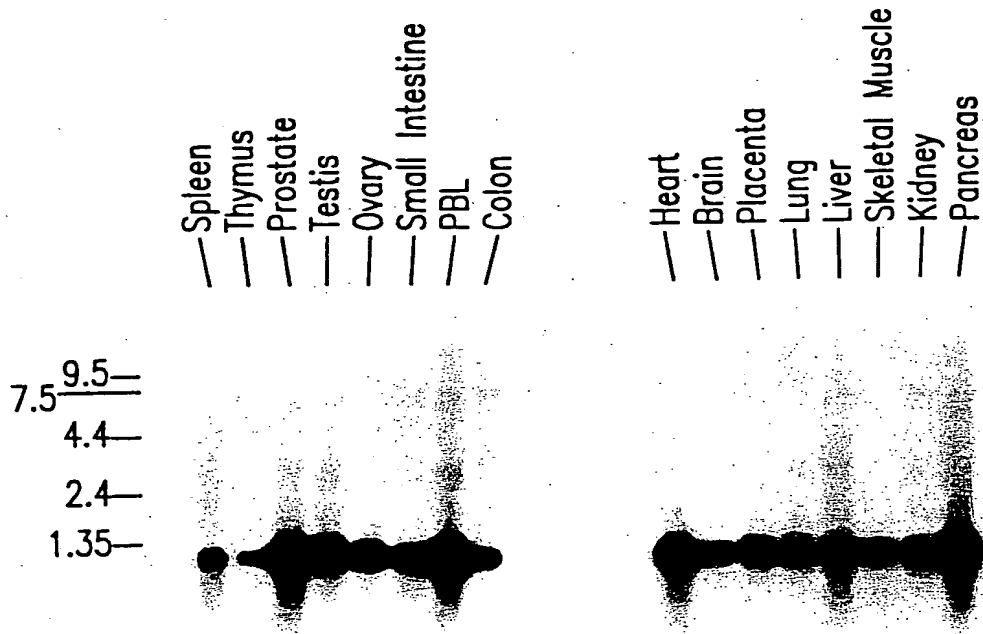


FIG.36B

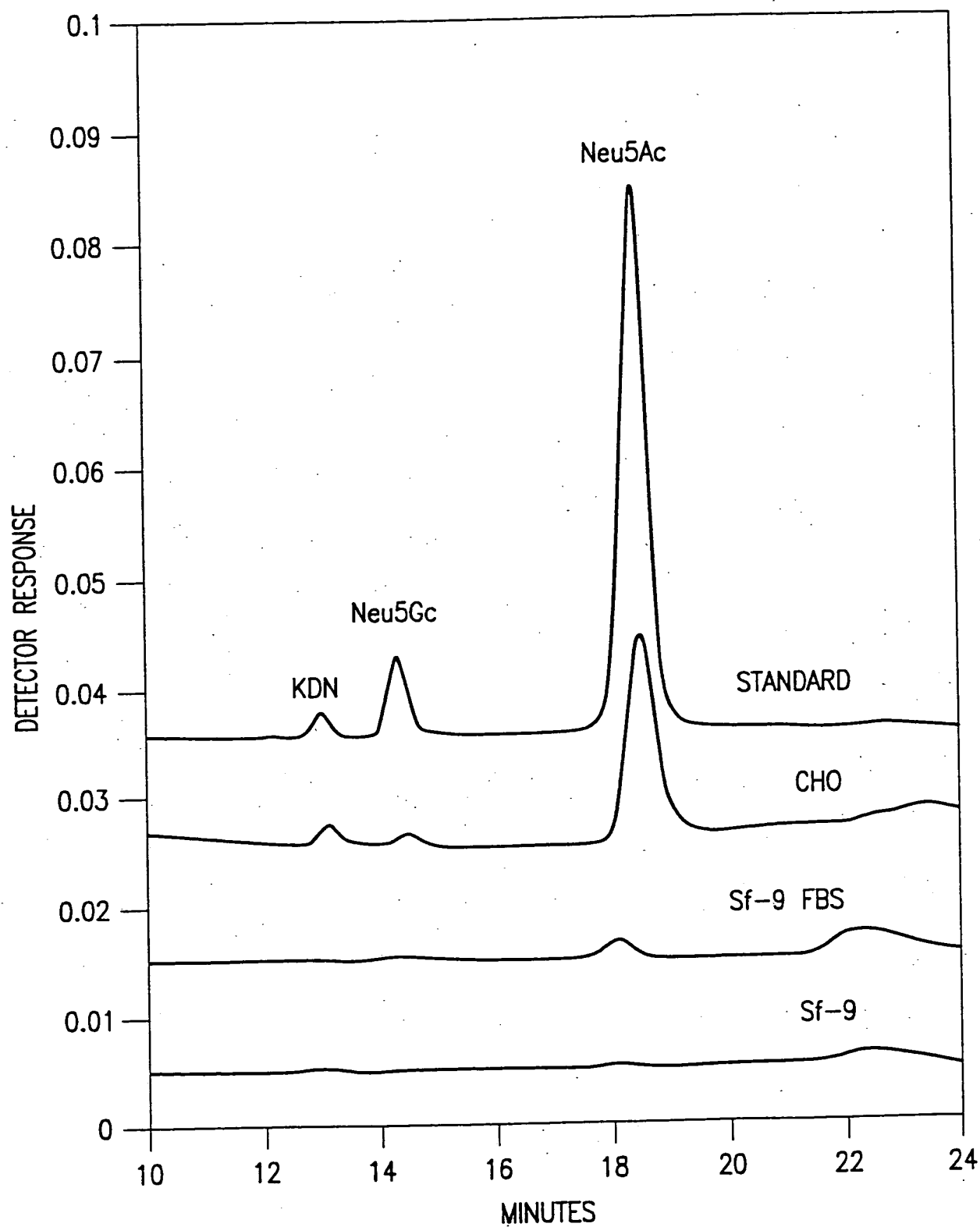


FIG. 37A

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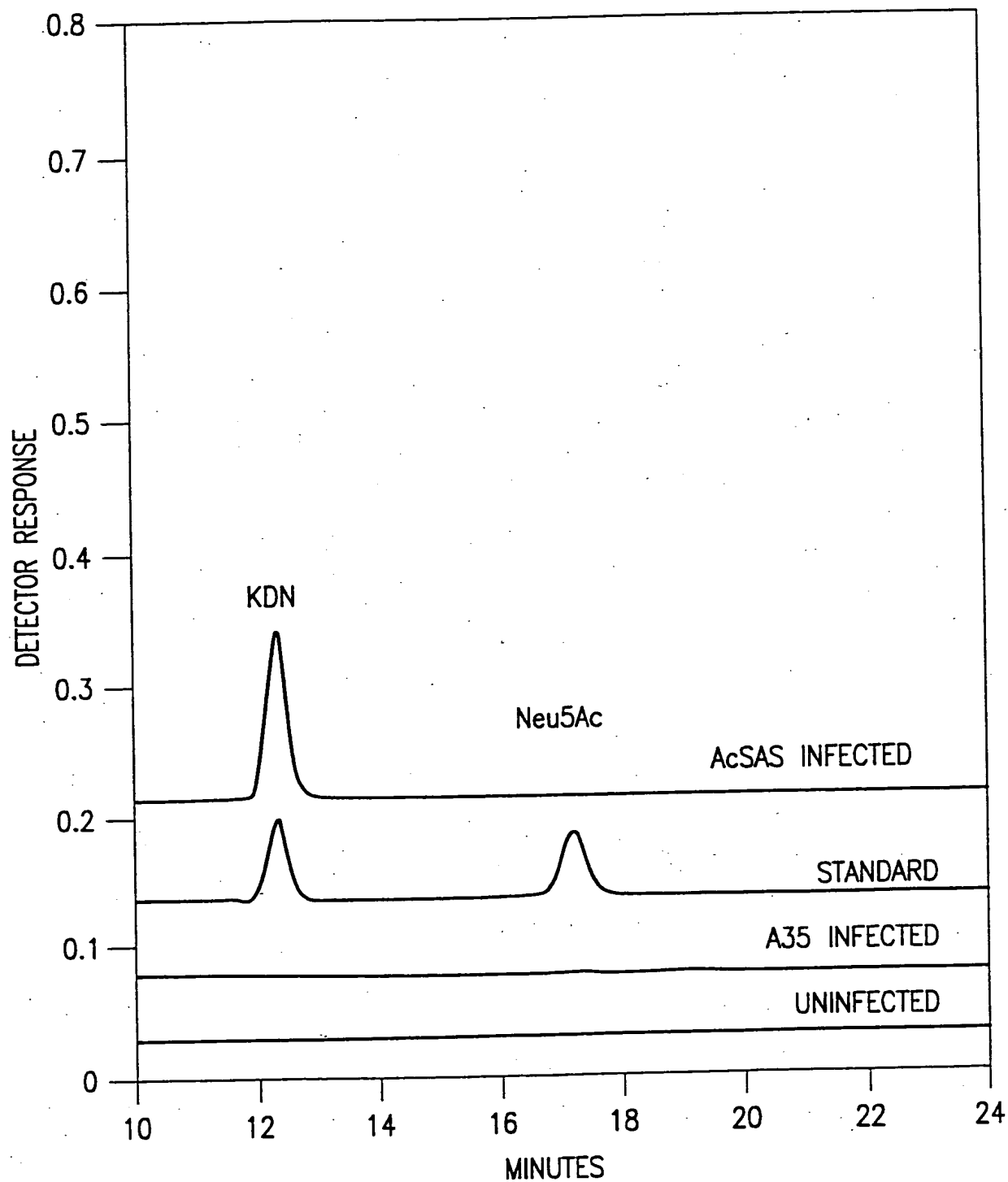


FIG. 37B

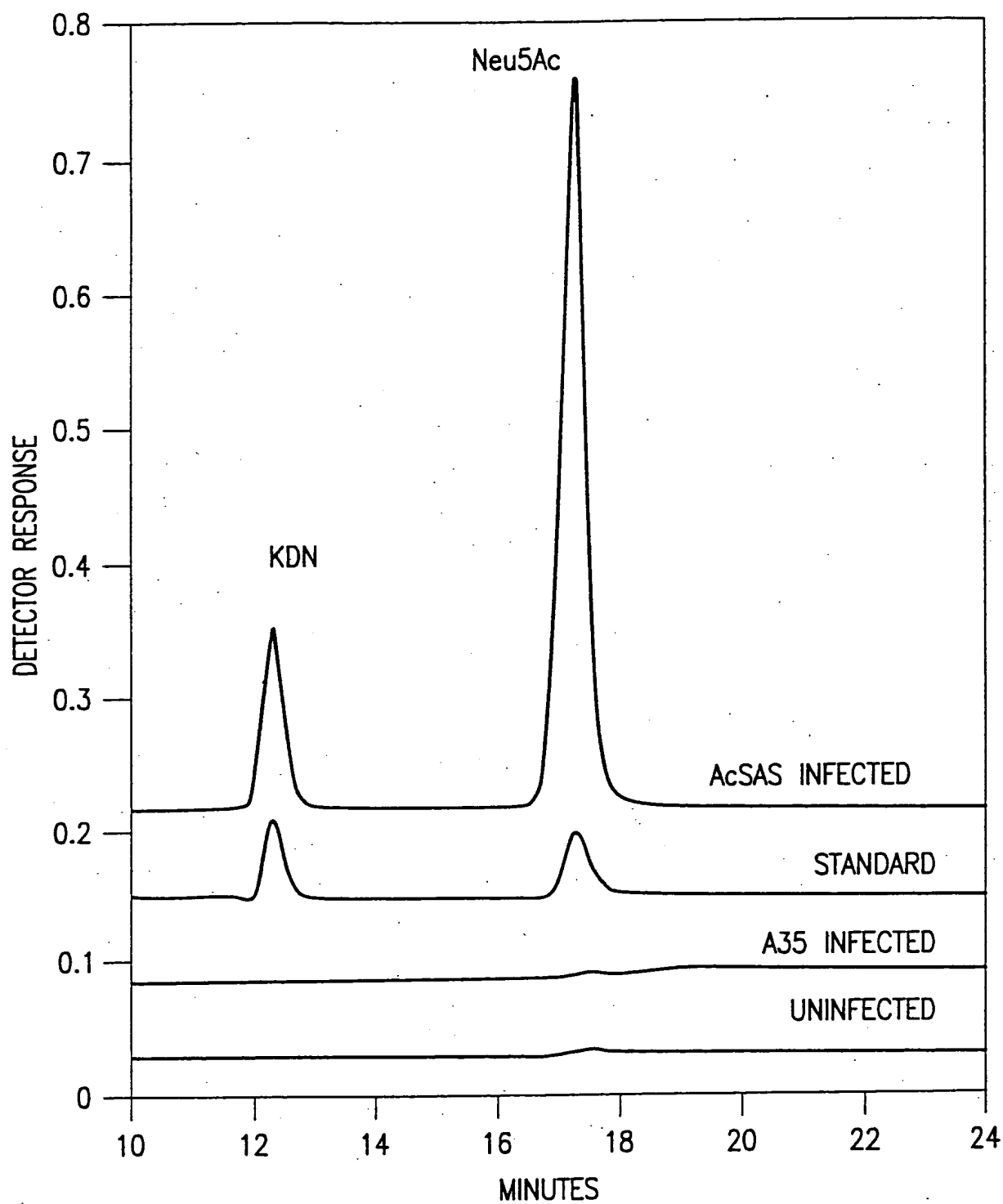


FIG. 37C

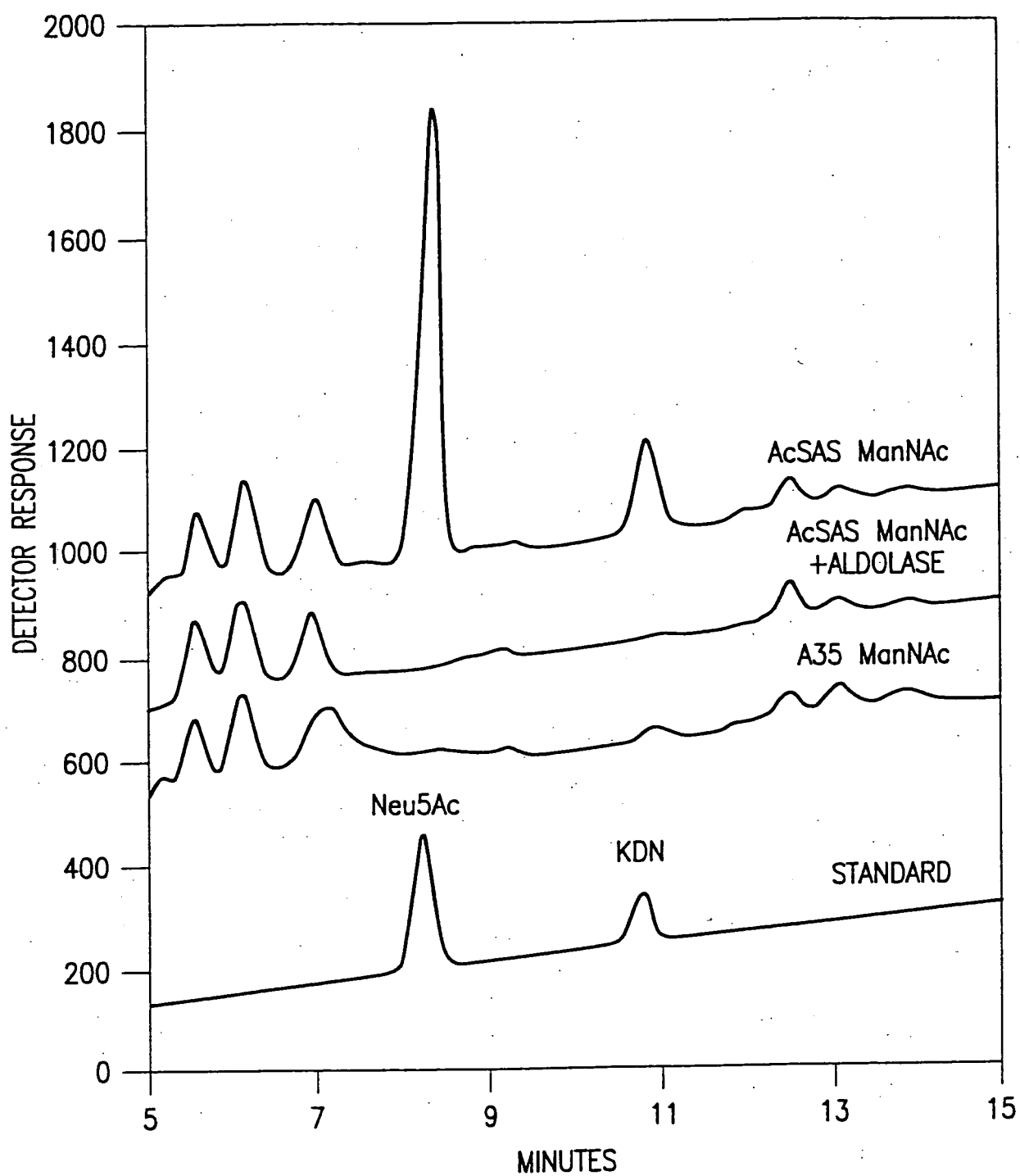


FIG. 37D

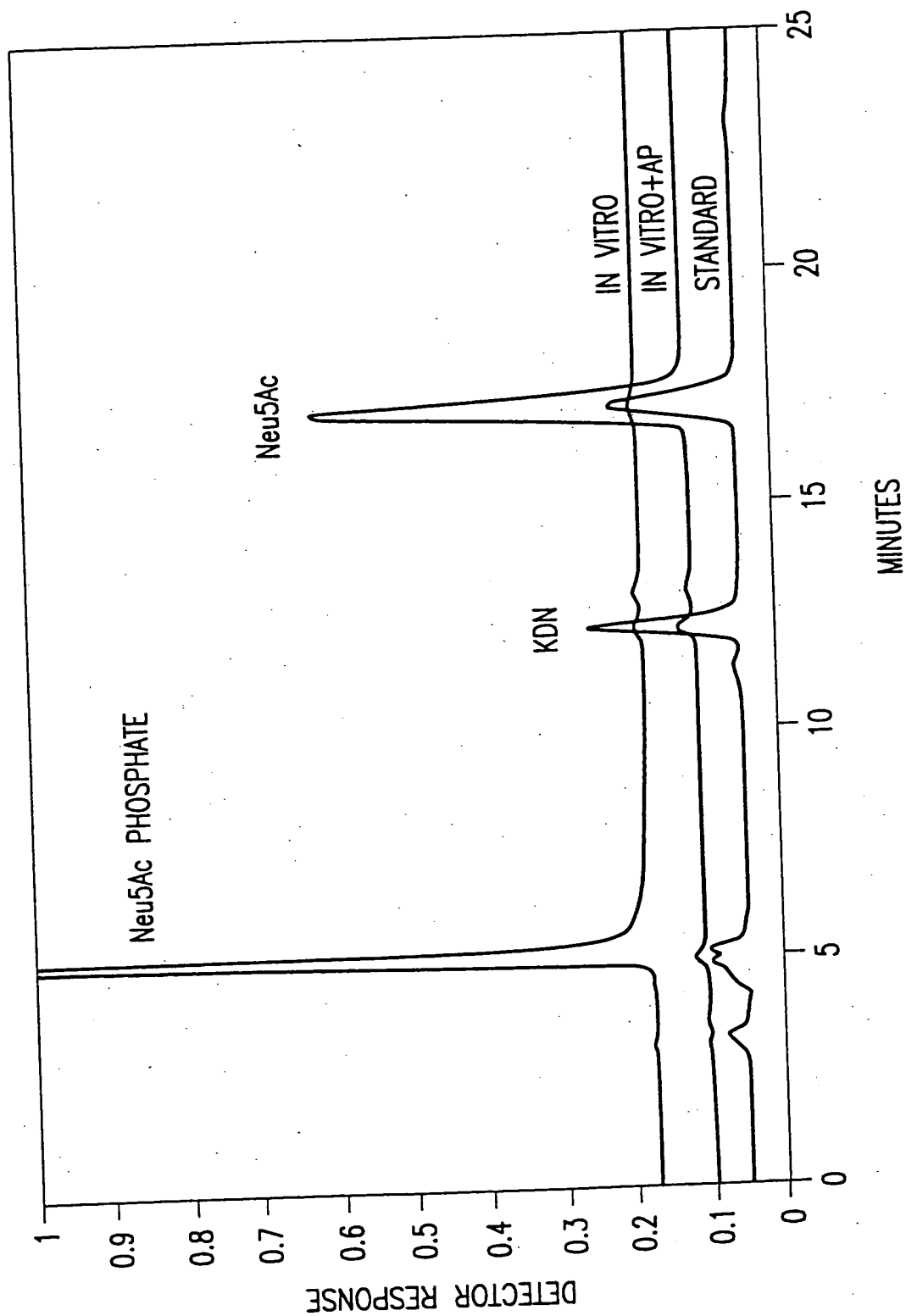


FIG. 38A

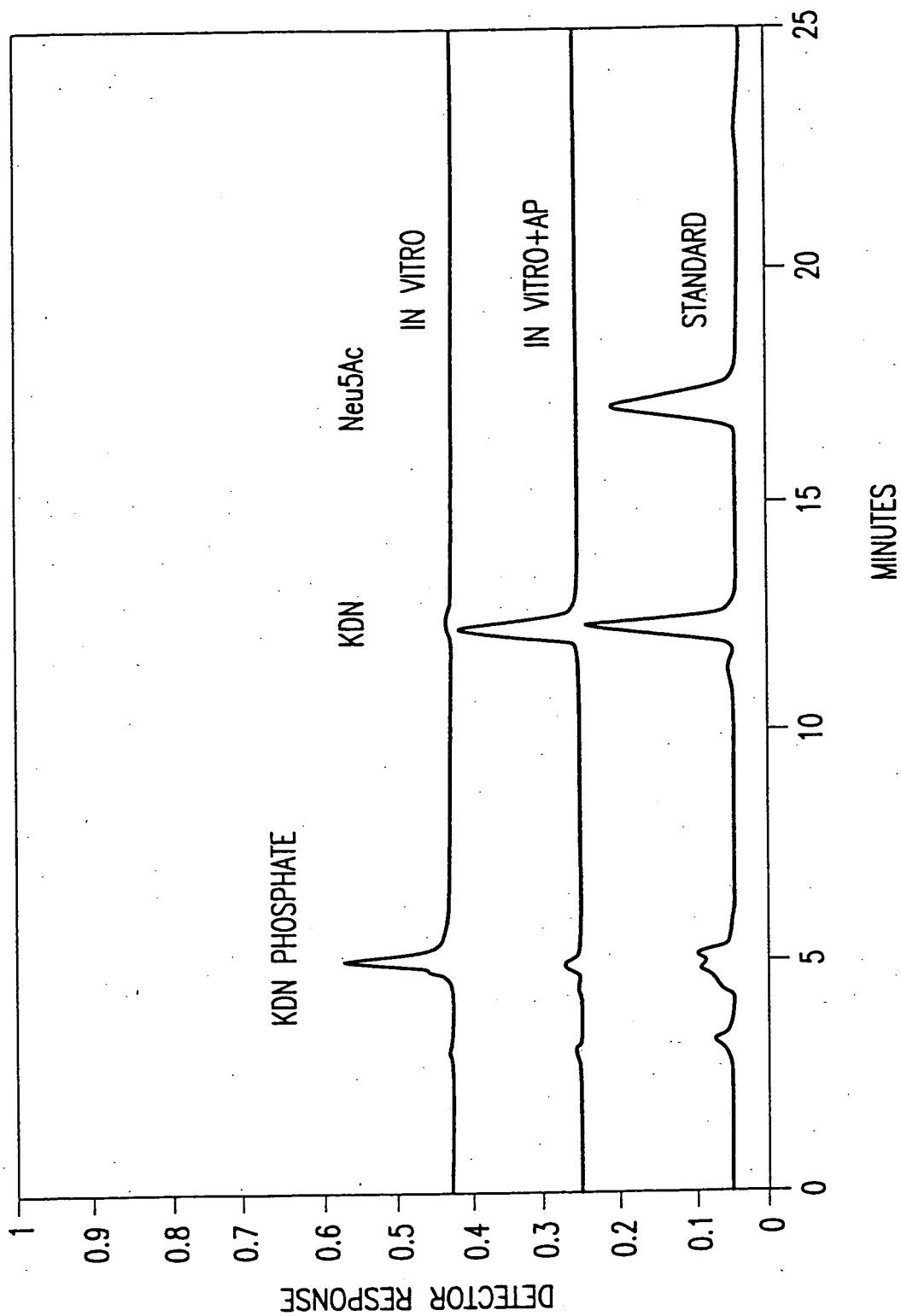


FIG. 38B

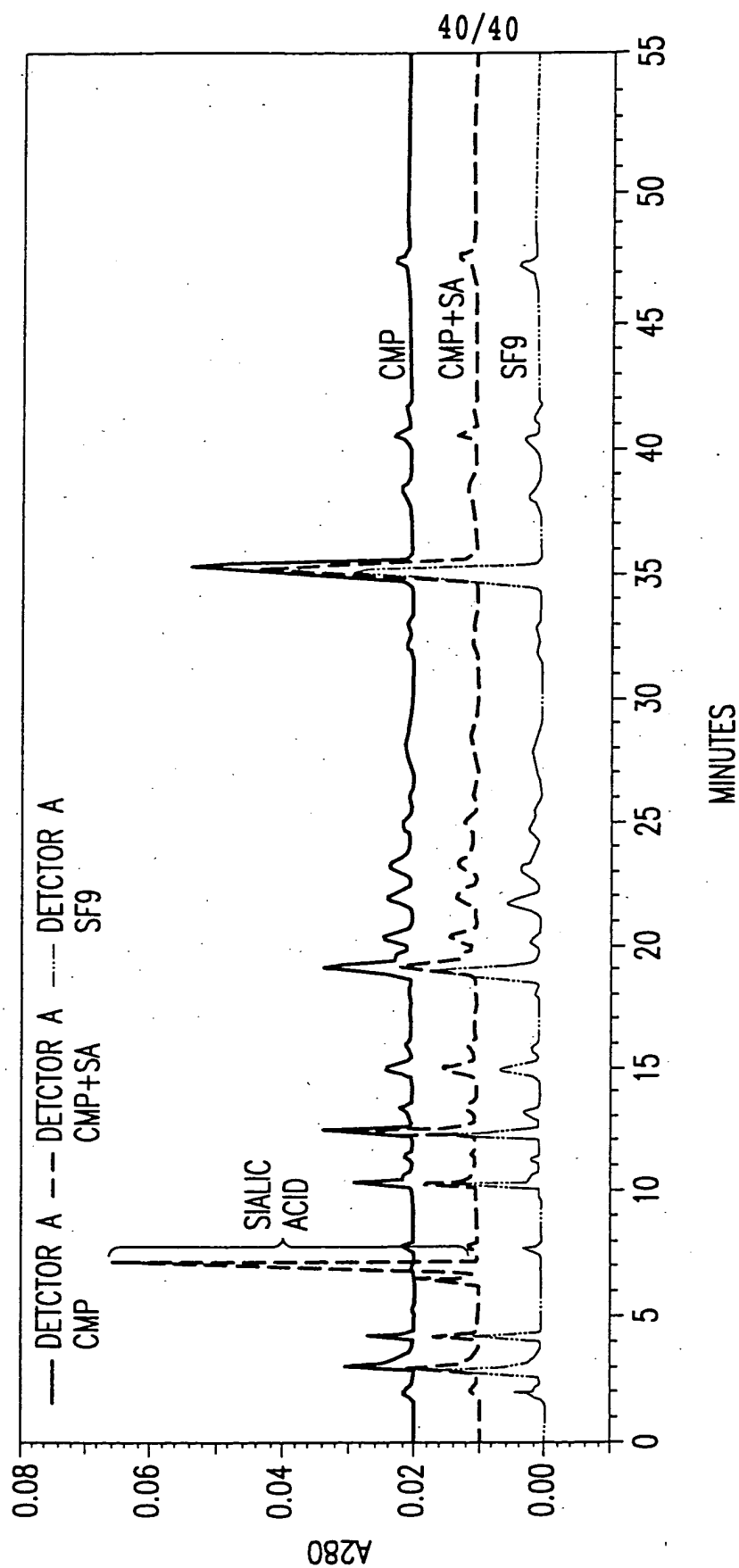


FIG. 39